

DRAFT

U.S. Application No. 09/965,553

Attorney Ref. No.: 08411-030002

05/12/03

PROPOSED NEW CLAIM

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XX. The isolated nucleic acid of claim 56,

wherein said pol gene comprises:

at least a portion of a plant integrase sequence, wherein said integrase sequence comprises a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid having at least 70% identity to the sequence shown in SEQ ID NO:9, wherein said identity can be determined using the DNAsis computer program and default parameters;

(b) a nucleic acid having the sequence shown in SEQ ID NO:9;

(c) a nucleic acid that encodes an amino acid having at least 75% identity to the sequence shown in SEQ ID NO:10, wherein said identity can be determined using the DNAsis computer program and default parameters;

(d) a nucleic acid that encodes an amino acid having the sequence shown in SEQ ID NO:10; and

(e) a nucleic acid having a sequence fully complementary to (a), (b), (c), or (d);

at least a portion of a plant reverse transcriptase sequence, wherein said reverse transcriptase sequence comprises a nucleic acid sequence selected from the group consisting of:

(f) a nucleic acid having at least 70% identity to the sequence shown in SEQ ID NO:11, wherein said identity can be determined using the DNAsis computer program and default parameters;

(g) a nucleic acid having the sequence shown in SEQ ID NO:11;

(h) a nucleic acid that encodes an amino acid having at least 79% identity to the sequence shown in SEQ ID NO:12, wherein said identity can be determined using the DNAsis computer program and default parameters;

(i) a nucleic acid that encodes an amino acid having the sequence shown in SEQ ID NO:12; and

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- (j) a nucleic acid having a sequence fully complementary to (f), (g), (h), or (i); and
- at least a portion of a plant RNaseH sequence, wherein said RNaseH sequence comprises a nucleic acid sequence selected from the group consisting of:
- (k) a nucleic acid sequence having at least 70% identity to the sequence shown in SEQ ID NO:15, wherein said identity can be determined using the DNAsis computer program and default parameters;
- (l) a nucleic acid having the sequence shown in SEQ ID NO:15;
- (m) a nucleic acid sequence that encodes an amino acid sequence having at least 90% identity to the sequence shown in SEQ ID NO:16, wherein said identity can be determined using the DNAsis computer program and default parameters;
- (n) a nucleic acid sequence that encodes an amino acid having the sequence shown in SEQ ID NO:16; and
- (o) a nucleic acid having a sequence fully complementary to (k), (l), (m), or (n);
- wherein said env gene comprises at least a portion of a plant envelope sequence, wherein said envelope sequence comprises a nucleic acid sequence selected from the group consisting of:
- (p) a nucleic acid having at least 50% identity to the sequence shown in SEQ ID NO:5, wherein said identity can be determined using the DNAsis computer program and default parameters;
- (q) a nucleic acid having the sequence shown in SEQ ID NO:5;
- (r) a nucleic acid that encodes an amino acid having at least 30% identity to the sequence shown in SEQ ID NO:6, wherein said identity can be determined using the DNAsis computer program and default parameters;
- (s) a nucleic acid that encodes an amino acid having the sequence shown in SEQ ID NO:6; and

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(t) a nucleic acid having a sequence fully complementary to (p),
(q), (r), or (s);
and wherein said isolated nucleic acid further comprises:
a nucleic acid having the sequence shown in SEQ ID NO:4; and
a nucleic acid comprising the sequence shown in SEQ ID NO:3 or
the complement of the sequence shown in SEQ ID NO:3, wherein said nucleic acid
encodes a plant retroviral polypurine tract.

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